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ABSTRACT

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MATHEMATICAL REPRESENTATIONS OF DEVELOPMENT THEORIES

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ABSTRACT

In this paper we explore the consequences of particular stage linkage structures for the evolution of a population. We first argue the importance of constructing "dynamic" models of developmental theories and show through a series of examples the implications of various stage connections for population movements. In discussing dynamic models, one thrust of our comments is to identify the sorts of process features about which assumptions must be made in order to convert a static theory about stage connections (the sort of specification commonly presented in life-span psychology) into a dynamic model. A second focus of our discussion concerns inverse problems: how to utilize a model formulation so that the stage linkage structure may be recovered from survey data of the kind collected by developmental psychologists.

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I. INTRODUCTION

Although time, usually in the guise of age, is a crucial variable in developmental psychology, it is the case that formal models of developmental phenomena rarely have the character of dynamic representations, in the sense of mimicking the evolution of an empirical process through time. The analytic procedures employed most extensively by life-span psychologists are factor analysis, regression, analysis of variance, scaling, clustering, and variants of these methods (see, for instance, Nesselroade and Reese 1973). These are powerful techniques for identifying variables that are central to the course of development in a particular substantive area (e.g., intellectual maturation, acquisition of moral values). Also, when applied to panel data, the procedures can yield insights into how the salience of key variables shifts over the life cycle, or over a portion thereof (e.g., stages in infancy, youth, adulthood).

These analytic methods do not, however, lead to dynamic formulations of developmental theories, which can be useful in testing predictions from a theory about the evolution of an empirical process, or in comparing the implications of competing explanations. By a dynamic formulation we mean a representation which incorporates into the mathematics the main assumptions about a developmental phenomenon and is specified in such a way that the relevant variables, and their postulated interrelations, are functions of time or subject's age. In this sense, like the empirical process, it too

constitutes an evolving system. As a simple illustration of such a model, consider the following statements of alternative evolutionary mechanisms:

(A) The growth of a process at each instant is proportional to its potential for future growth.

(B) The growth of a process at each instant is proportional to the product of its current size and its potential for future growth.

These statements might be proposed as competing explanations of the manner by which information is diffused in a population of size N. In formulation (A), it matters not how many persons y(t) know the information of concern at instant t; only those yet to hear, numbering N-y(t), are salient to the diffusion rate. If the information were propagated by a mass media source, such as radio or television, rather than by interpersonal communication, this model might apply. Formulation (B), in comparison, is consistent with a process in which those already aware of the information "infect" the uninitiated through contact and conversation. Assuming that the informed and the uninformed mix randomly, the variable governing the evolution of the process would be $y(t)\left[N-y(t)\right]$, which measures the rate at which individuals from the two groups come into contact.

The evolutionary mechanisms, (A) and (B), can be represented by the differential equations (1) and (2), respectively,

$$\frac{dy(t)}{d(t)} = k_1\left[N - y(t)\right] \qquad y(0) = 0 \qquad (1)$$

$$\frac{dy(t)}{d(t)} = k_2 y(t)\left[N - y(t)\right], \qquad y(0) = 1 \qquad (2)$$

where k_1 and k_2 are constants which adjust for the time unit (e.g., day, year) used in the measurements.[1] Equations (1) and (2) have for solutions (3) and (4),

$$y(t) = N(1 - e^{-k_1 t}) \qquad (3)$$

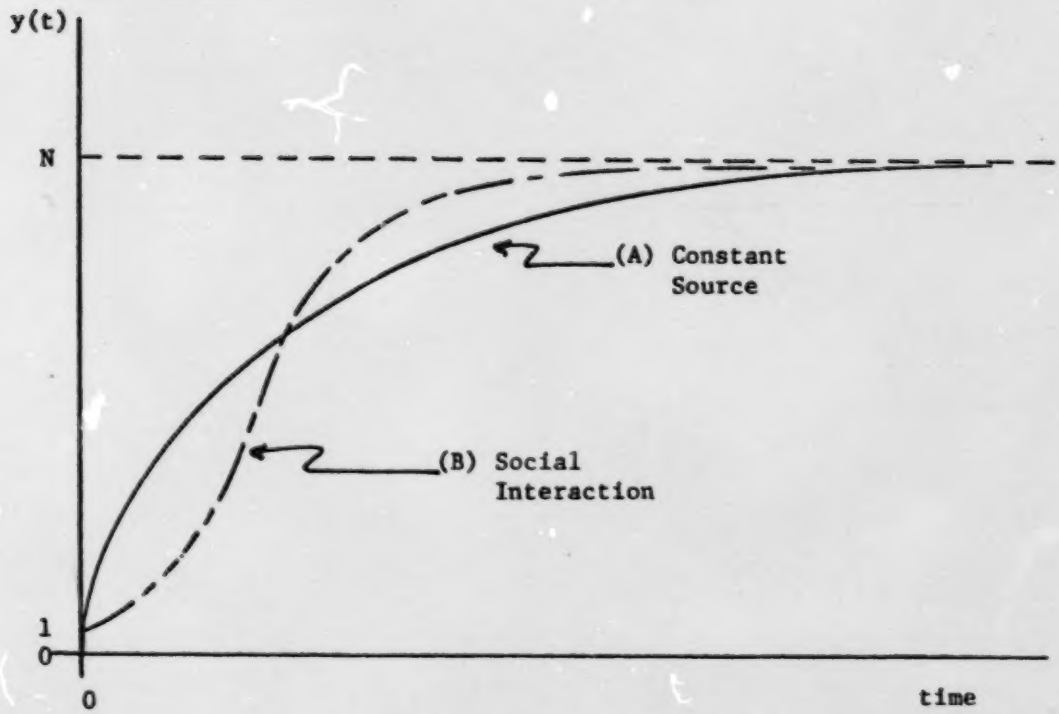
$$y(t) = \frac{Ne^{Nk_2 t}}{N-1+e^{Nk_2 t}} \qquad (4)$$

which predict the different evolutionary paths displayed in Figure 1.

These formulations are "dynamic" in that time appears explicitly as a variable; they are process "models" in that the predicted value of y(t) evolves according to the assumptions of a particular theory. If a researcher has data on the time course of an empirical process, he could test whether equation (3), (4), or a specification of an equivalent sort best approximates his observations. By this exercise it is often possible to select among competing explanations of the mechanism underlying a developmental process. Indeed, these very models have been applied by Coleman, Katz, and Menzel (1957) to data on drug adoptions by physicians (also see Coleman 1964, pp. 43-45). They concluded that the drug acquisition pattern by socially integrated MD's is best represented by a logistic curve (implying mechanism [B]), while isolated MD's adopt according to the constant source model (mechanism [A]), as they are influenced principally by drug advertisements in trade journals To our knowledge, although developmental psychologists emphasize ontogenetic processes and employ the imagery of an evolutionary system, few attempts have been made to translate their theories into formal models of the above sort.

In this paper, we describe the formulation of dynamic models where the objective is to test developmental theories against data or ascertain the consequences of particular assumptions about the structure of a process. To

Figure 1. Illustrative Growth Curves for Diffusion via Social Interaction and Diffusion from a Constant Source[a]



[a] N = population size; y(t) = number aware of the information at time t.

delimit our task, we focus on the sort of mathematics that is appropriate for studying qualitative change. As a result, the tools we introduce are pertinent to theories which postulate stage sequences, a variety of explanation with considerable precedent in developmental psychology (Piaget 1960; Kohlberg 1968; Ausubel and Sullivan 1970). To the degree possible we have organized this paper with a view toward substantive issues and have concentrated on the translation of theoretical specifications into mathematical formalism; the reader usually is referred elsewhere for mathematical details and estimation procedures. The organization of the paper is as follows: In the next section we introduce a class of models that is suitable for studying evolutionary processes that incorporate the notion of stage. In section III we describe how particular stage theories can be cast in the framework of the general model. In section IV we relax several requirements of the basic model so that it can more realistically represent developmental phenomena.

II. THE CONCEPT OF DEVELOPMENT STAGES AND A MATHEMATICAL FORMULATION OF STAGE PROGRESSIONS

Stage sequences have been postulated for a variety of developmental processes--the evolution of moral behavior (Kohlberg 1973), cognition (Piaget 1954), personality (Loevinger 1966), and motor skills (Shirley 1933), to cite but a few topics. There also exist diverse formulations of stage models in the literature of life-span psychology. These differ with respect to the presumed sources of the stages and with regard to the rules governing movement between them. In regard to stage origins, some authors have emphasized maturational considerations, in which individuals are viewed as programmed genetically for particular behaviors or abilities to emerge (Gesell 1954). The specification of psychosexual stages, keyed to biological activation of the sex glands, provides an illustration (Kohlberg 1973, p. 181). Others

view stages as arising from interactions with the social environment. Kohlberg (1968, pp. 1016-1024), for example, contends that experience with the cultural and physical world is necessary for cognitive stages to take the shapes they do. Still other researchers have adopted the position that stages are a useful research construct around which to discuss development, without insisting that they have an empirical existence (Kaplan 1966; Reese 1970).

We shall not discuss further the very important issues concerning the etiology of stages, but will focus instead on the mathematical representation of theories about stage connections and on the consequences of various linkage structures for the evolution of individuals among the stages. Formulations of stage connections in a developmental process differ according to whether the progression is viewed as unilineal or multilineal, whether stages in the sequence can be skipped, and whether regression to an earlier level is possible. A second set of considerations pertinent to the structure of developmental theories concerns the age specificity of a stage and the related matter of the variability of duration in a stage. For discussions of these topics in the context of particular substantive processes, the reader is referred to Emmerich (1968) and Kessen (1962).

To develop the mathematical apparatus for ascertaining the implications of particular stage connections, we discuss both the simplest prototype of a stage theory (for concreteness) and the general mathematical formulation.[2] Consider, then, a developmental progression consisting of n stages, in which the linkage is unilineal and there is no possibility of stage skipping or regression. An example of such a structure, with n equal to 5, is presented in panel A of Figure 2; henceforth this model is referred to as example 1. It will be convenient to also have available a matrix representation of the stage linkages. For an arbitrary n-stage structure, we define a matrix M,

$$M = \begin{bmatrix} m_{11} & m_{12} & \cdots & m_{1n} \\ m_{21} & \cdots & \cdots & m_{2n} \\ \vdots & & & \vdots \\ m_{n1} & \cdots & \cdots & m_{nn} \end{bmatrix} \qquad (5)$$

whose elements are m_{ij} = {probability of transferring from stage i to stage j when a transition occurs}, where $0 \leq m_{ij} \leq 1$, and $\sum_{j=1}^{n} m_{ij} = 1$. These restrictions on the elements of M ensure that each row of the matrix constitutes a probability distribution. We require, in addition, that $m_{ii} = 0$ for each stage i which is not an absorbing state of the process; that is, from which individuals can exit. This means we exclude the possibility of within-stage transitions, a type of move which is undefined in most developmental theories. Also, we set $m_{ii} = 1$ for each stage which is an absorbing state of the process. This is done for mathematical convenience and, as we shall see, carries no substantive implications. In the particular case of the unilineal progression (Figure 2, panel A), we have the further requirements on M: $m_{i,i+1} = 1$, and $m_{ij} = 0$ otherwise (except that $m_{55} = 1$). This matrix, M_1, is reported in panel B of Figure 2.

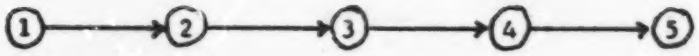
To this point, though matrix M conveys important structural information about the process, the description of the stage progression is a static representation. To elaborate the model we must indicate how stage transition events occur. At a general level of description we assume that the time τ_k spent by an individual in stage i follows some probability distribution ,

$$\text{Prob}_i(\tau_k < t | \tau_1, \ldots, \tau_{k-1}) \qquad (6)$$

where $\tau_1, \ldots, \tau_{k-1}$ report the sojourn times in earlier stages. Our imagery,

Figure 2. Representation of a Simple Unilineal Stage Structure

a. Diagram of Stage Linkages



b. Matrix Representation[a] of the Stage Linkages[b]

$$M_1 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

---

[a] Each row of M_1 is a vector of destination probabilities. Thus, if an individual were in stage one before a transition, the row one entries would pertain and they indicate movement to stage two with probability equal to 1.

[b] The main diagonal entries are set equal to zero (with the exception of row 5) to indicate that a "move" is not defined apart from a stage transition; i.e., there is no notion of movement within a stage. The main diagonal entry of row 5 is set equal to 1 because this stage is an absorbing state ($m_{5j} = 0$ for $j \neq 5$) and the definition of M_1--see text--requires $\sum_j m_{5j} = 1$.

therefore, is the following. An individual originates in stage i at the beginning of the process, $t_0 = 0$. He remains there for an interval τ_1, specified by a distribution function $\text{Prob}_i(\tau_1 < t)$, and then transfers to stage j with probability m_{ij}. He remains in this stage for a period τ_2, specified by a conditional probability distribution $\text{Prob}_j(\tau_2 < t|\tau_1)$, then transfers to stage k with probability m_{jk}; and so forth.[3] The process continues until some absorbing state is reached, at which point the evolution is terminated. The time path for the unilineal progression associated with the stage linkages of matrix M_1 is presented in Figure 3.

Several further assumptions are necessary to complete the specification of the model. One matter concerns the relevance of an individual's past movement history to the course of his subsequent evolution among the stages. We assume,

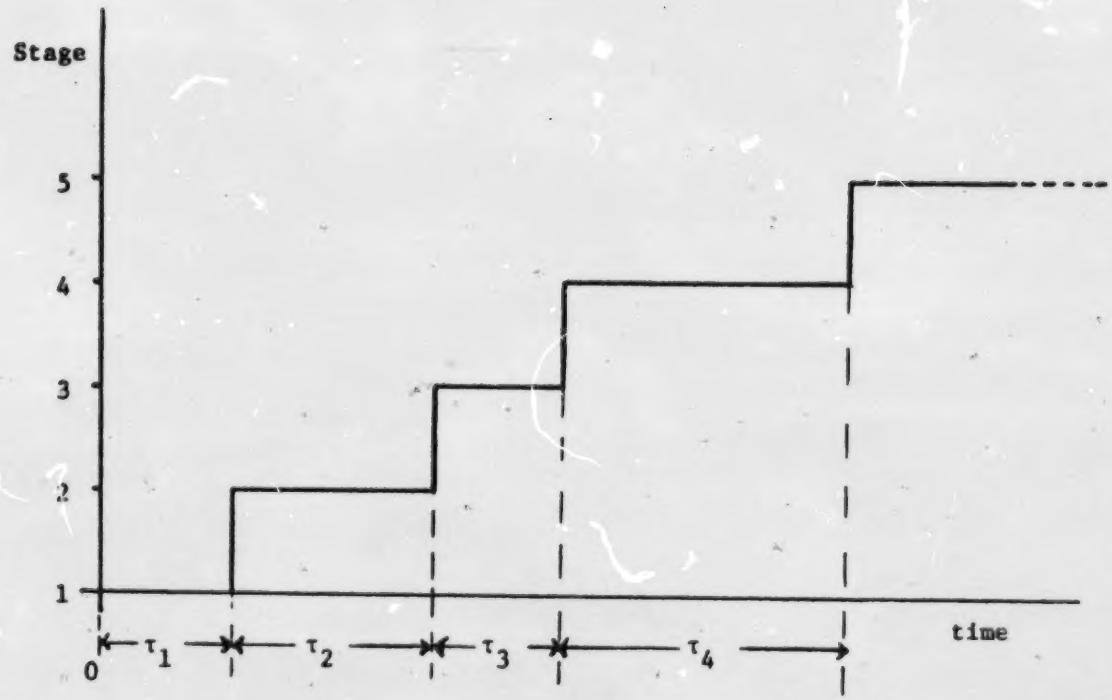
(i) knowledge of current stage conveys all information that is relevant to forecasting future movements.

Stated technically, if $m_{ij,ab...f}$ = {probability of moving from stage i to stage j at the occurrence of a transition, given prior sojourns in stages a, b,...f}, then

$$m_{ij,ab...f} = m_{ij}.$$

(This assumption is superfluous in the current example of a unilineal progression since there is only one possible path, but it is relevant to the evolution of a population in less restrictive models.) We indicate in the next section that this specification has been employed in descriptions of stage linkages in developmental psychology.

Figure 3. A Sample Path Description Corresponding to the Unilineal Stage Structure of Figure 2.



[a]It is assumed that there are five stages, which must be traversed sequentially. τ_i is the value of a random variable and denotes the sojourn time for an individual in stage i. Stage 5 is an absorbing state of the process.

For an initial baseline class of models, we further assume,

(ii) the sojourn time in stage i is independent of previous sojourn times and is exponentially distributed; that is,

$$\text{Prob}_i(\tau_k < t | \tau_1, \ldots, \tau_{k-1}) = \text{Prob}_i(\tau_k < t) = F_i(t) = 1-e^{-\lambda_i t} . \qquad (7)$$

Use of the exponential distribution amounts to specifying that the probability of departing from stage i during the infinitesimal interval t + dt, conditional on being in stage i at time t, equals

$$\frac{f_i(t)dt}{1 - F_i(t)} = \frac{\lambda_i e^{-\lambda_i t} dt}{1-\left(1-e^{-\lambda_i t}\right)} = \lambda_i dt$$

where $f_i(t)$ is the density function corresponding to $F_i(t)$. This result, in turn, indicates that the probability of leaving stage i is independent of duration in the stage, and is tantamount to specifying an absence of aging, so new entrants have the same likelihood of departing as individuals who have been in the stage for some period of time. The parameter, λ_i, incidentally, has an interpretation as the rate of movement out of stage i; consequently, $1/\lambda_i$ equals the expected duration in stage i.

Finally, we require that

(iii) if the data pertain to the movements of a population, rather than to the transitions of a single individual, the population is homogeneous with respect to the structure of the evolutionary process.

This does <u>not</u> mean that all persons have the same duration τ_i in stage i, but that τ_{ic}, the time spent in stage i by individual c, follows the single exponential distribution $F_i(t) = 1-e^{-\lambda_i t}$. Stated less formally, duration in a stage

is a random variable with the underlying distribution of holding times the same for all individuals. Similarly, where alternative destinations are available to persons in stage i, homogeneity means that all have the same list of probabilities for making the various transitions, not that they move identically.

It is worth dwelling on the conceptual status of the preceding assumptions. The question of the structure of M is a familiar topic to developmental psychologists, since stage theories are commonly specified at this level. Assumptions (i) to (iii) can be viewed as "side conditions," aspects of the process to which researchers have generally not been sensitive, though see Kessen (1970) and Emmerich (1968) for provocative comments on precisely these matters. What is made evident by formulating a dynamic model is that development theorists must address these auxiliary questions if complete models are to be specified. The particular assumptions we have made constitute a gross simplification of reality; this is especially true of specification (ii), which postulates an absence of duration effects, and specification (iii), which postulates population homogeneity. These assumptions do, however, provide a convenient starting point from which to consider more realistic formulations, which are developed in the next sections.

We now wish to convey the implications of assumptions (i) to (iii) for the movements of individuals among the stages. We denote by $p_{ij}(t)$ the probability that an individual in stage i at time 0 moves to stage j by time t. (This probability differs from m_{ij} in that the latter refers to movement proclivities at the occurrence of a transition, not over widely spaced time intervals.) With this specification in hand, the evolution of a population among the stages is described by the system of integral equations,

$$p_{ij}(t) = \delta_{ij} e^{-\lambda_i t} + \sum_k \int_0^t \lambda_i e^{-\lambda_i u} m_{ik} p_{kj}(t - u)du \qquad (8)$$

$0 \leq i, j \leq n$

where $\delta_{ij} = 1$ if $i = j$, and 0 otherwise. This expression, known as the backward equations for a continuous-time Markov process (Feller 1971, p. 484), is amenable to the following interpretation: (1) When $i \neq j$, $p_{ij}(t)$ consists of the sum of products of three factors: the probability of a first departure from stage i at time u, the probability of a stage i to stage k transition at that instant, and the probability of transferring to stage j by some combination of moves in the interval t - u. The summation is over all intermediate stages k and over all time divisions u in the interval (0, t). (2) When $i = j$, in addition to the above term, there is the possibility of not transferring out of stage i during (0, t). This probability is given by the first term.

If we represent by P(t) the matrix of elements $p_{ij}(t)$,

$$P(t) = \begin{bmatrix} p_{11}(t) & \cdots & p_{1n}(t) \\ \vdots & & \vdots \\ p_{n1}(t) & \cdots & p_{nn}(t) \end{bmatrix}$$

$0 \leq p_{ij}(t) \leq 1$, $\sum_j p_{ij}(t) = 1$, then the integral equations (8) have the convenient solution,

$$P(t) = e^{\Lambda[M - I]t}, \qquad P(0) = I. \tag{9}$$

In this representation Λ is a diagonal matrix,

$$\Lambda = \begin{bmatrix} \lambda_1 & & 0 \\ & \lambda_2 & \\ & & \ddots \\ 0 & & \lambda_n \end{bmatrix}$$

whose entries are the reciprocals of the expected duration times in each stage, I is the identity matrix, and M is the array specified in equation (5) which

describes the pattern of movement between the stages. Further, by the expression e^A, A an arbitrary square matrix, we mean the power series in A,

$$e^A = \sum_{n=0}^{\infty} \frac{A^n}{n!} \tag{10}$$

which can be evaluated by standard numerical methods (see, e.g., Gantmacher [1960]).

It is useful to recapitulate what is accomplished by this mathematical formulation. The matrix P(t) relates the distribution of a population among stages at time t to its distribution at time 0, in the sense that a typical entry, $p_{ij}(t)$, represents the probability of moving from stage i to stage j during the interval (0,t). The model is "dynamic" in that P(t) is a function of time; with the passage of time P(t) describes the evolution of the population among the stages. Equation (9) shows how the matrix P(t) is built up from the arrays M and Λ. However, while this equation is useful as a calculating formula, the logic of the process is conveyed more adequately by the integral equations (8).

To illustrate this model in the setting of a simple unilineal progression (matrix M_1 of Figure 2) we must specify average waiting times in stages 1,2,3, and 4. We assume these to be .5, 1, 2, and 5 years, respectively. Consequently, we have for matrix Λ,

$$\Lambda = \begin{bmatrix} 2 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .5 & 0 & 0 \\ 0 & 0 & 0 & .2 & 0 \\ 0 & 0 & 0 & 0 & \lambda_5 \end{bmatrix} \tag{11}$$

where the choice of λ_5 is arbitrary. (Since stage 5 is an absorbing state, the notion of waiting time to a departure has no meaning. Mathematically, $[M - I]_{55} = [m_{55} - I] = [1-1] = 0$, so λ_5 bears no influence on the calculations.) Now, from M_1, Λ, and I, we have

$$\Lambda(M_1 - I) = \begin{bmatrix} -2 & 2 & 0 & 0 & 0 \\ 0 & -1 & 1 & 0 & 0 \\ 0 & 0 & -.5 & .5 & 0 \\ 0 & 0 & 0 & -.2 & .2 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} . \qquad (12)$$

For the illustrative times t = 1, 2, and 4 years, we obtain, from (9), for P(t),

$$P(1) = \begin{bmatrix} .1353 & .4651 & .3263 & .0691 & .0041 \\ .0000 & .3679 & .4773 & .1438 & .0110 \\ .0000 & .0000 & .6065 & .3537 & .0398 \\ .0000 & .0000 & .0000 & .8187 & .1813 \\ .0000 & .0000 & .0000 & .0000 & 1.0000 \end{bmatrix} \qquad (13)$$

$$P(2) = \begin{bmatrix} .0183 & .2340 & .4641 & .2482 & .0354 \\ .0000 & .1353 & .4651 & .3394 & .0602 \\ .0000 & .0000 & .3679 & .5041 & .1281 \\ .0000 & .0000 & .0000 & .6703 & .3297 \\ .0000 & .0000 & .0000 & .0000 & 1.0000 \end{bmatrix} \qquad (14)$$

and

$$P(4) = \begin{bmatrix} .0003 & .0360 & .2881 & .4843 & .1913 \\ .0000 & .0183 & .2340 & .5079 & .2398 \\ .0000 & .0000 & .1353 & .3233 & .5413 \\ .0000 & .0000 & .0000 & .4493 & .5507 \\ .0000 & .0000 & .0000 & .0000 & 1.0000 \end{bmatrix} . \qquad (15)$$

These values of P(t) describe the evolution of individuals among the stages, subject to the assumptions about the process structure detailed above. The entries of $p_{ij}(t)$ refer to proportions[4] of the population who have moved between particular stages in the relevant time interval. For example, according to the entries in the top row of P(1), if observations are taken one year apart, we would expect 13 percent of the population in stage 1 at time 0 to still be there, 46 percent to have moved to stage 2, and 33 percent to have reached stage 3. By comparison, over a four-year interval, less than 1 percent would remain in stage 1, 48 percent would have reached stage 4, and 19 percent would be in the terminal stage of the process.

The results from the three calculations reveal that, even though the progression is unilineal with all individuals characterized by the same parameters, if observations were taken on the population at two time points, t=0 and $t=t_1$, the array $^5\hat{P}(t_1)$ might be interpreted as evidence for a more complex theory, such as one permitting stage skipping or population heterogeneity in the rate or pattern of movement. Further, the correspondence between the matrix constructed from the population locations at two time points, $\hat{P}(t_1)$, and the rule governing stage transitions, M_1, decreases with time. Thus, different researchers observing the same population at two time points, but with different spacing intervals, might draw contrary conclusions about the stage linkage structure even though the single mechanism, M_1 of Figure 2, governs its evolution. Only with a formal model of the process could one hope to uncover its underlying structure.

III. MODELS OF MORE ELABORATE STAGE THEORIES

The matrix M contains structural information about stage linkages. Since theories of development are commonly posed at the level of specifying this array, flexibility in incorporating a variety of specific formulations would appear to be an important feature of a general framework for describing evolutionary behavior. In this section we focus on the issue of translating stage theories into M-matrices, and illustrate the evolution of P(t), the transition matrix for a population based on its locations at times 0 and t, under alternative specifications of M. As we have noted, auxiliary information about the process, concerning the distribution of waiting time intervals and the form of population heterogeneity, is required for a full description of a dynamic model. In the next section we therefore elaborate upon these "side conditions" and outline ways in which our initial assumptions can be relaxed.

No technical difficulties arise in reformulating the continuous-time Markov model to accommodate more elaborate theories of stage linkages than the structure in Figure 2. We illustrate the procedure with a few examples.[6]

(2) A unilineal progression which permits stage skipping. The formulation of such a structure is diagrammed in Figure 4, panel A; its translation into an M-matrix is reported in panel B. The principal new feature is that, supplementing the deterministic sequence of Figure 2, it is now possible to move directly from stage 2 to stage 4 and from stage 3 to stage 5, when a transition out of the relevant origin location takes place. We must also specify the probabilities of following the alternate paths. In the present example, lacking information as to the relative magnitudes of the various probabilities, we assume all destinations to be equally likely; that is, we prescribe $m_{23} = m_{24} = .5$, and $m_{34} = m_{35} = .5$. In practice, estimates of the transition probabilities would be assigned on the basis of theory or from observation on the empirical process.

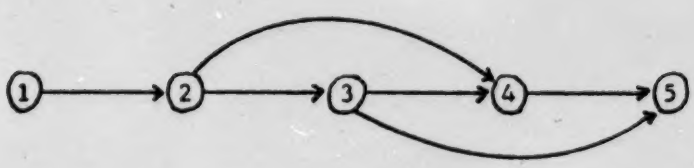
Using matrix M_2, together with the Λ array of equation (11), whose entries describe the rate of movement by individuals out of each stage, we obtain for P(1) and P(4), from equation (9),

$$P(1) = \begin{bmatrix} .1353 & .4651 & .1632 & .2012 & .0352 \\ .0000 & .3679 & .2387 & .3177 & .0757 \\ .0000 & .0000 & .6065 & .1768 & .2166 \\ .0000 & .0000 & .0000 & .8187 & .1813 \\ .0000 & .0000 & .0000 & .0000 & 1.0000 \end{bmatrix} \qquad (16)$$

$$P(4) = \begin{bmatrix} .0003 & .0360 & .1440 & .4104 & .4093 \\ .0000 & .0183 & .1170 & .3964 & .4683 \\ .0000 & .0000 & .1353 & .2617 & .6030 \\ .0000 & .0000 & .0000 & .4493 & .5507 \\ .0000 & .0000 & .0000 & .0000 & 1.0000 \end{bmatrix} . \qquad (17)$$

Figure 4. Representation of a Unilineal Progression in which Stage Skipping is Permitted

a. Diagram of Stage Linkages



b. Matrix Representation of the Stage Linkages[a]

$$M_2 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .5 & .5 & 0 \\ 0 & 0 & 0 & .5 & .5 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

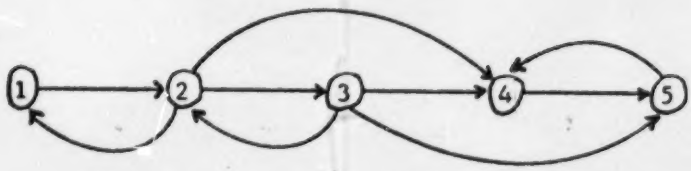
[a]All destination stages corresponding to an origin location are assumed to occur with equal probability. See notes to Figure 2 for additional details on interpretation of M_2.

These P(t) arrays are the transition matrices a researcher should expect to observe if the stage locations of individuals are surveyed one year or four years apart, assuming that the population evolves according to the linkage specification M_2 together with the auxiliary conditions outlined in the preceding section. The entries are different from those obtained with the simple unilineal progression (equations 13 and 15), yet the same pattern of zero's and non-zero's is present, and without a formal model of the evolution of the process a researcher would be unable to predict the different implications of these structures.

(3) A unilineal progression with stage skipping and the possibility of regression. We now superimpose on the linkage structure the possibility of reverting to an earlier stage. This arrangement is diagrammed in Figure 5, panel A, in which we have provided for the possibility of backward flows from stage 2 to stage 1, from stage 3 to stage 2, and from stage 5 to stage 4. The M-matrix corresponding to this model is reported in panel B. Again, where multiple destinations correspond to an origin stage, we have arbitrarily assigned equal values to the m_{ij}'s. There is one additional alteration in M_3, in comparison with the M-matrices of earlier examples. Because there now exists a possibility of regressing from the terminal stage to an earlier level, $m_{55} \neq 1$. To maintain our conceptual imagery, in which within-stage transitions are undefined, we set $m_{54} = 1$ and $m_{55} = 0$. Note that the former value does not imply a high rate of departure from stage 5, since the rate of movement is controlled by λ_5. It only means that all transitions from stage 5 are directed to stage 4.

Figure 5. Representation of a Unilineal Progression in which Stage Skipping and Regression to an Earlier Level are Permitted

a. Diagram of Stage Linkages



b. Matrix Representation of the Stage Linkages[a]

$$M_3 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ .33 & 0 & .34 & .33 & 0 \\ 0 & .33 & 0 & .34 & .33 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix}$$

[a]All destination stages corresponding to an origin location are assumed to occur with equal probability. See notes to Figure 2 for additional details on interpretation of M_3.

To obtain P(t) we use M_3 and Λ in conjunction with equation (9). Here the element λ_5 in equation (11) is no longer arbitrary, as movement out of stage 5 is a possibility. We shall assume that such reversions are rare, and hence specify the average waiting time to a transition from stage 5 to be eight years; that is, $\lambda_5 = .125$. With these assumptions, we obtain for our illustrative calculations at t = 1, 4,

$$P(1) = \begin{bmatrix} .2043 & .5240 & .1153 & .1374 & .0190 \\ .0871 & .4758 & .1742 & .2217 & .0411 \\ .0094 & .0858 & .6215 & .1461 & .1371 \\ .0000 & .0000 & .0000 & .8292 & .1708 \\ .0000 & .0000 & .0000 & .1067 & .8933 \end{bmatrix} \quad (18)$$

$$P(4) = \begin{bmatrix} .0330 & .1560 & .1652 & .4025 & .2433 \\ .0259 & .1246 & .1500 & .4174 & .2820 \\ .0135 & .0739 & .1846 & .3542 & .3738 \\ .0000 & .0000 & .0000 & .5523 & .4477 \\ .0000 & .0000 & .0000 & .2798 & .7202 \end{bmatrix} \quad (19)$$

If we compare the P(1) matrices and the P(4) matrices from the three examples [i.e., equations (13), (16), (18) and (15), (17), and (19)], we can acquire a fair idea of the implications of different stage interconnections for the evolution of a population among the statuses. We also emphasize the fact that if a population were surveyed at two time points, especially widely spaced time points, it may not be obvious from inspecting the empirically determined transition array, $\hat{P}(t_1)$, as to the structure of the stage linkages (matrix M) which generated the observations. We will return to the issue of identifying the correct structure and recovering matrix M when the observations on a process are widely spaced; first we conclude this discussion on translating theoretical specifications of stage linkages into M-matrices with a couple of examples of multilineal sequences that have been described in the developmental psychology literature.

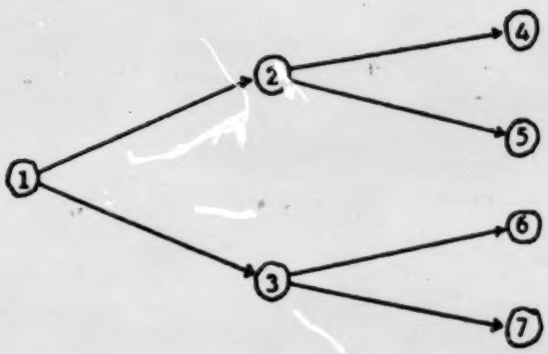
(4) A divergent multiple progression (Van Den Daele 1969, Figures 2, 4). This stage linkage structure has the diagrammatic representation of Figure 6, panel A; its corresponding M-matrix is presented in panel B. Because stages 4-7 are specified to be terminal states of the process, the corresponding rows of M_4 have 1's in the main diagonal. Van den Daele provides no discussion of waiting time distributions to departure from the various stages; hence the model remains incomplete as an evolutionary process.

(5) A convergent multiple progression (Van Den Daele 1969, Figure 2). This stage sequence is depicted in Figure 7, panel A, and its associated M-matrix is reported in panel B. In this instance, the structure consists of a collection of deterministic unilineal progressions, the specific sequence for an individual being contingent upon his entry stage. Note also that the assumption of irrelevance of past history, which is posited in this formulation, is one of the side conditions we have required (assumption [i] in the preceding section). In particular, this specification appears in the fact that knowledge of the path by which one has reached stage 5 (or stage 6) is of no value in forecasting, or understanding, an individual's subsequent movements. Van Den Daele (1969) discusses several additional models of stage linkages, such as "partially convergent, divergent progression," and "partially divergent, convergent progression." As the procedure in converting flow structures into M-matrices should be evident at this point, discussions of these specifications are not presented.

To recapitulate, subject to several side conditions, we have shown that it is possible to construct formulations of a range of developmental phenomena which mimic the evolutionary character of the observed process. With such a model one can forecast the movements of a population among the stages. By

Figure 6. Representation of a Divergent Multiple Progression[a]

a. Diagram of Stage Linkages



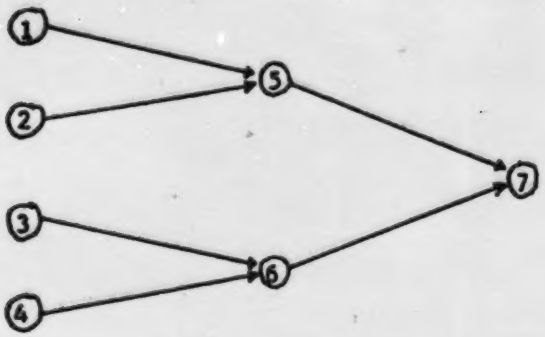
b. Matrix Representation of the Stage Linkages

$$M_4 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & .5 & .5 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & .5 & .5 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

[a]Source: Van Den Daele (1969, Figures 2, 3).

Figure 7. Representation of a Convergent Multiple Progression[a]

a. Diagram of Stage Linkages



b. Matrix Representation of the Stage Linkages[a]

$$M_5 = \begin{bmatrix} 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

[a]Source: Van Den Daele (1969, Figure 2).

carrying out the requisite calculations for different specifications of the stage linkages, and comparing the predictions, it is possible to ascertain the ways in which rather complex theories produce divergent implications and design testing schemes which maximize the possibility of rejecting one or another formulation as a description of the empirical process. Of equal importance, it is often possible to work backwards, starting with observations on the stage locations of a population at a few widely spaced time points, and derive the structure of the stage linkages compatible with the data.

An inverse problem. Until this point we have assumed that observations have been made on an empirical process in a way such that M and Λ can be estimated directly from the data, or that theories are available which specify the values of their entries, and have sought to derive the evolution of the process subject to the presumed structure. In developmental psychology, it is not uncommon for a researcher to have many observations on a few individuals (e.g., Piaget 1954). Such a data collection scheme approximates "sample path information," a complete history on movements and waiting times of the sort illustrated in Figure 3. Detailed observations on a few subjects is a research strategy not without its costs, however. One learns little about the frequency of rare events (e.g., regression to an earlier stage, stage skipping, rare development paths) and acquires only the most rudimentary knowledge about the variation of duration times in a stage. It is therefore not surprising that investigators who rely on this approach tend to be oriented to uncovering universal rules (e.g., Piaget 1960) rather than to elucidating individual differences and ascertaining the variety of developmental patterns.

Partly because of the limitations of small data sets, it is becoming increasingly common to employ survey methods, in which a large population, sometimes thousands of individuals, is observed (or interrogated) at a very few time points (e.g., Baltes and Nesselroade 1972). The spacing intervals in such panel studies are usually wide, often one or more years elapses between interviews, so it is not unusual for some subjects to have made multiple moves while others have made one or zero shifts between stages. The transition matrices which can be constructed directly from such observations are P(t)-arrays, rather than M-arrays, and the stage linkages may not be readily discernable. Indeed, determination of the movement structure which underlies the evolution of the population can be a difficult task.

One approach to ascertaining the stage linkages from survey data involves consideration of the "inverse problem" to the mathematical formulation of the evolutionary model (equation 9). Stated formally, we have available the matrix $\hat{P}(t_1)$, constructed from observations on the stage locations of individuals at times 0 and t_1. The typical entry in this matrix is $\hat{p}_{ij}(t_1) = n_{ij}(t_1)/n_{i.}$, where $n_{i.}$ = {number of individuals in stage i at time 0} and $n_{ij}(t_1)$ = {number of persons who started in stage i at time 0 and are in stage j at time t_1}. We wish to inquire whether it is possible to recover a unique M-matrix for the process and, where the answer is affirmative, we wish to estimate this matrix.

The first step in solving the inverse problem is to take the logarithm of both sides of equation (9),

$$Q = \Lambda[M - I] = \frac{1}{t_1} \ln \hat{P}(t_1) \quad . \tag{20}$$

Just what we mean by the logarithm of matrix $\hat{P}(t_1)$, the conditions under which a solution to equation (20) will exist, and the circumstances under which the solution will be unique, are complex issues which are discussed at length in

Singer and Spilerman (1976). Assuming we can obtain a valid and unique Q-matrix from these calculations, a second task, separating M from Λ, still remains. In many instances, though, this matter is of little concern, since the pattern of zeros and non-zeros in Q and M - I will be identical and development theories are often posed at the level of identifying permissible transitions. Moreover, because zeros are typically present in many main diagonal cells of M in models of developmental structures, a complete or near complete separation between M and Λ can frequently be effected.

We conclude this section with an example of the calculations associated with the inverse problem. Suppose observations taken on a population at times 0 and t_1 have produced the transition matrix,

$$\hat{P}(t_1) = \begin{bmatrix} .0224 & .2633 & .2402 & .1261 & .3479 \\ .0063 & .1758 & .2460 & .1735 & .3983 \\ .0216 & .0288 & .3758 & .5060 & .0679 \\ .0365 & .0745 & .0288 & .6794 & .1809 \\ .0005 & .0960 & .0460 & .0177 & .8397 \end{bmatrix} . \qquad (21)$$

Such data would appear to be consistent with a variety of evolutionary mechanisms. From inspection of $\hat{P}(t_1)$ we do know that regression to some earlier stage must be possible, otherwise all entries below the main diagonal would be zero. Little else about the structure of M, however, can be inferred from inspection of $\hat{P}(t_1)$. Indeed, because of the sizable non-zero elements in most cells of the matrix, a researcher might conclude that direct transitions are possible between most pairs of stages.

If we are willing to assume that matrix $\hat{P}(t_1)$ was generated by a continuous-time Markov process; that is, via the evolution of the structure $P(t) = e^{\Lambda(M-I)t}$, for some matrices Λ and M which satisfy the definitional restrictions enumerated in connection with equations (5) and (9), we can solve for $\Lambda(M-I)t_1$ using equation (20). This yields the array,

$$\Lambda(M - I)t_1 = \begin{bmatrix} -4. & 4. & 0. & 0. & 0. \\ 0. & -2. & 1. & 0. & 1. \\ 0. & 0. & -1. & 1. & 0. \\ 0.20 & 0. & 0. & -0.40 & 0.10 \\ 0. & 0.25 & 0. & 0. & -0.25 \end{bmatrix} . \qquad (22)$$

In this instance Λt_1 and M can be separated by employing the following argument. From our earlier examples we know that a main diagonal element m_{ii} of M will equal zero if any off diagonal entry in the same row, m_{ij}, is different from zero. According to equation (22), each row of matrix M must have at least one non-zero off diagonal element; therefore $m_{ii} = 0$ for all values of i. With this information we can obtain Λt_1 uniquely,

$$\Lambda t_1 = \begin{bmatrix} 4 & 0 & 0 & 0 & 0 \\ 0 & 2 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & .4 & 0 \\ 0 & 0 & 0 & 0 & .25 \end{bmatrix} \qquad (23)$$

and solving for M provides the structure M_4 reported in Figure 8, panel A. The schematic representation of the stage linkages implied by M_4 is shown in panel B, in which probabilities of the various moves have been appended to the paths.

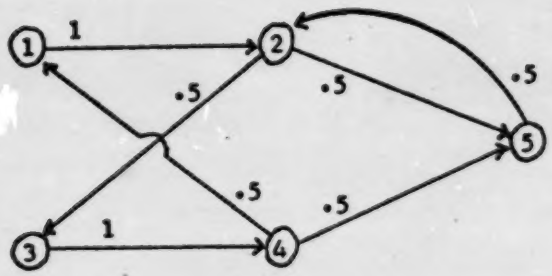
The point to be emphasized is that it is not apparent from inspecting matrix $\hat{P}(t_1)$ in equation (21) that the underlying stage linkages are those reported in Figure 8, nor would any static analytic procedure be likely to lead a researcher to the correct conclusion. What is necessary is to construct a model of the evolution of the process and solve the implied inverse problem for the parameters which correspond to the particular data set. (In the present example, we have assumed that the underlying model is a continuous-time Markov process [i.e., specifications (i)-(iii) of the preceding section] and have solved for the matrices Λt_1 and M which are compatible with the observed

Figure 8. Stage Sequence Structure Implied by $\hat{P}(t_1)$ in Equation (21)[a]

a. M-matrix[b]

$$M_4 = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .5 & 0 & .5 \\ 0 & 0 & 0 & 1 & 0 \\ .5 & 0 & 0 & 0 & .5 \\ 0 & 1 & 0 & 0 & 0 \end{bmatrix}$$

b. Diagram of Stage Linkages[c]



[a]The process is assumed to evolve according to a continuous-time Markov formulation.

[b]Entries indicate the probability of a stage i to stage j move when a transition takes place.

[c]Probabilities of the various transitions are attached to the appropriate paths.

array (t_1), in that they would have given rise to this array if the postulated evolutionary process were approximately correct.

IV. ALTERNATIVE SPECIFICATION OF THE SIDE CONDITIONS

In this section we discuss relaxing two of the more burdensome specifications of the model, in the sense that they are likely to be inappropriate as characterizations of developmental processes. We first consider the requirement that the duration intervals in a stage must follow an exponential distribution (assumption (ii) of section II). Following these comments we turn to the requirement that the population be homogeneous with respect to the process parameters Λ and M (assumption (iii)).

More general waiting times than exponential. The exponential distribution is frequently employed in the literature of reliability theory to describe duration intervals in a system state (stage in the current application). It has the advantages of being mathematically tractible and approximating reality in situations where the probability of a state change is uninfluenced by aging or time in the state. For example, if the process states are "alive" and "not alive," then over the middle age ranges of many animal species, the age-specific mortality rate is relatively constant and the duration intervals (in the "alive" state) are reasonably well captured by the exponential distribution. Similarly, when mortality results from exogeneous events--accidents--the distribution of ages at failure can often be approximated by the exponential.

In a great many situations in social research, however, we know that proneness to changing state is a function of duration. In particular, this has been suggested with respect to residence location (McGinnis, 1968) and employment affiliation (Ginsburg, 1971). In these applications it has been argued that the duration-specific departure rate decreases with time, giving rise to the phenomenon of "cumulative inertia"--the longer an individual remains in a state the less likely he is to leave in the immediate future.

The substantive explanations for a declining departure rate involve the growing investment an individual has made, with duration, in friendships (in the first instance) and in seniority in his place of work (in the second). There is no mathematical reason, however, to assume a declining departure rate in choosing $F_i(t)$, and in other substantive contexts a different specification may be more appropriate. For a superb review of stochastic models incorporating the notion of duration dependence, see Hoem, 1972.

A convenient way to generalize the Markov model to accommodate a variety of duration-time distributions is to begin with the integral equation representation for transition probabilities. Equation (8) is a special case of the formulation,

$$p_{ij}(t) = \delta_{ij}[1 - F_i(t)] + \sum_k \int_0^t f_i(u) m_{ik} p_{kj}(t-u)du \qquad 0 \leq i,j \leq n \qquad (23)$$

in which the terms are identical with those of the earlier equation except that $f_i(u)$ replaces the exponential density, $\lambda_i e^{-\lambda_i u}$, and $F_i(t)$ [the distribution function corresponding to $f_i(t)$], replaces $[1 - e^{-\lambda_i t}]$. A theoretically appropriate choice may now be made for $F_i(t)$.

As an illustration, one candidate for $F_i(t)$, in the case of a declining departure rate, is the two-parameter family of functions

$$F_i(t) = 1 - e^{-\lambda_i t^{\gamma_i}} \qquad \lambda_i > 0;\ 0 < \gamma_i < 1 . \qquad (24)$$

Here the probability of departing from state i during the infinitesimal interval $(t, t + dt)$, conditional on the process being in state i at time t, equals

$$\frac{f_i(t)}{1-F_i(t)} = \frac{(\lambda_i \gamma_i t^{\gamma_i - 1}) e^{-\lambda_i t^{\gamma_i}} dt}{e^{-\lambda_i t^{\gamma_i}}} = \lambda_i \gamma_i t^{\gamma_i - 1} dt .$$

Because of the restriction on γ_i in equation (24), $t^{\gamma_i - 1}$ is a decreasing function of time, and the declining failure rate aspect of the distribution is evident.

The general formulation (23) for duation time distributions and transitions between states generates a class of models known as semi-Markov processes. These generally do not have simple representations for the matrices P(t) analogous to equation (9), and the solution of the systems of equations (23) requires numerical integration methods.

Population heterogeneity. To this point we have assumed that the matrices Λ and M of equation (9) are identical for all individuals. This does not mean that all persons move identically since the process is probabilistic; it does imply, though, that individual level characteristics are unrelated to the structural parameters of the process. In other words, homogeneity means that considerations of genetic makeup, intelligence, sensory stimulation, and other factors by which individuals differ from one another do not portend distinct evolutionary paths in the developmental process under consideration.

There is reason to believe, however, that individual differences are present in the course of development in many processes (Werner, 1957; Kohlberg, 1968, p. 1024). We therefore desire a formulation in which the movement pattern is parametrized in terms of variables which differentiate among persons. To construct a general specification of heterogeneity within the conceptual framework of a Markov process, we assume that, corresponding to equation (9), the stage transitions by individual c have the structure

$$P_c(t) = e^{\Lambda_c(M_c - I)t} . \qquad (25)$$

This formula indicates that each person is characterized by a pair of matrices,

Λ_c and M_c, and his evolution, in turn, is described by $P_c(t)$. Thus, our formulation begins with a separate Markov process for each individual.

This approach directs a researcher to identify the variables which describe heterogeneity; that is, to ascertain which factors account for individual differences in the matrices M and Λ. Thus, not only does a heterogeneity formulation lead to more realistic models of evolutionary processes, in that allowance is made for individual differences, but it stresses the analytic tasks of specifying the variety of developmental patterns in a population and ascertaining the attributes which make an individual more prone to following one set of paths rather than another.

One form of heterogeneity concerns the distribution of M-matrices in a population. Focusing on these arrays serves to emphasize individual differences in proneness to making particular moves when a transition takes place. We shall not discuss this form of heterogeneity in the present essay and direct the interested reader instead to McFarland (1970), Spilerman (1972a), and Singer and Spilerman (1974). A second form of heterogeneity stresses individual differences in the Λ-matrix, i.e., in the rates at which departures occur for persons in the various states. We conclude this section with a simple formulation of population heterogeneity in which it is assumed that the individual differences can be expressed in the latter way.

To simplify the discussion, we further require the non-zero entries in the diagonal matrix Λ to be equal for an individual; i.e., $\lambda_i = \lambda$ for all i. This means we are specifying identical departure rates from all states. As a result, equation (9) reduces to

$$P(t|\lambda) = e^{\lambda t(M-I)} \tag{26}$$

where $P(t|\lambda)$ denotes the transition matrix for an individual having a

rate of movement value equal to λ. We shall assume that equation (26) describes the evolution of an individual drawn at random from the population.

Heterogeneity is incorporated into the formulation by specifying a density function $g(\lambda)$ which describes the distribution of λ-values in the population. We now define the population-level transition matrix corresponding to times 0 and t to be

$$P(t) = \int_0^\infty P(t|\lambda)g(\lambda)d\lambda = \int_0^\infty e^{t\lambda(M-I)}g(\lambda)d\lambda \ . \qquad (27)$$

This formula expresses the population-level matrix as a weighted average of the individual-level arrays $P(t|\lambda)$, the weights reflecting the population proportions associated with particular λ-values.

To complete this specification of heterogeneity it is necessary to select a density function $g(\lambda)$ to describe the distribution of λ-values. One useful choice is the gamma family of functions ,

$$g(\lambda) = \frac{\beta^\alpha \lambda^{\alpha-1} e^{-\beta\lambda}}{\Gamma(\alpha)} \qquad \lambda > 0,\ \alpha > 0,\ \beta > 0 \qquad (28)$$

which is flexible enough to describe a variety of unimodal curves. With this selection of $g(\lambda)$, a convenient representation of the population-level matrix P(t) is obtained (Spilerman, 1972b, p. 608),

$$P(t) = \left(\frac{\beta}{\beta+t}\right)^\alpha \left[I - \frac{t}{\beta+t} M\right]^{-\alpha} \ . \qquad (29)$$

The transition probabilities (29) do not describe the evolution of a Markov

process; however, they do describe the movements of a population in which each individual follows a Markov model, with individual differences being specified by $g(\lambda)$ in equation (28).

In analogy with our earlier inverse problem discussion for Markov chains, the present formulation can be used with observations taken at widely spaced time points, 0 and t_1, together with estimates of α and β, to yield an estimate of the underlying transition mechanism M, according to the matrix equation

$$M = \frac{\beta+t_1}{t_1}\left[I - \frac{\beta}{\beta+t_1}\left(\hat{P}(t_1)\right)\right]^{-1/\alpha} . \qquad (30)$$

Thus, from observations of the sort collected in many surveys, even under an assumption of population heterogeneity in the rate of movement, it may be possible to recover the matrix of stage linkages which governs the evolution of the process.

V. CONCLUSIONS

In this paper we have explored the consequences of particular stage linkage structures for the evolution of a population. One thrust of our comments has been to identify the sorts of process features concerning which assumptions must be made in order to convert a static theory about stage connections into a dynamic model. A second focus in our discussion has centered on inverse problems; how to utilize a model formulation so that the stage linkage structure (matrix M) may be recovered from survey data of the kind usually collected by developmental psychologists.

We have presented only the most rudimentary sorts of stage structures. Indeed, even within the Markov framework we have limited our consideration to

a subset of these models; namely, those which are time-stationary (i.e., Λ and M are not functions of time). By this specification we have excluded the possibility of accommodating age-dependent transition laws, a consideration of substantial importance in developmental psychology. (An extension of the models discussed here to incorporate both age dependence and cohort effects is, however, a feasible undertaking but with an increase in mathematical complexity.) Further, all the models we have discussed entail a low dependence of future movements on the transition history of an individual, given his current stage.[7] Restrictions of these sorts are likely to be reasonable for some processes, unreasonable for others. Appropriate models of developmental phenomena must therefore be constructed from a list of known characteristics about an empirical process.

We also point out that the concept of stage merges with the notion of state as the number and sorts of permissible transitions is increased. "Stage" seems conceptually rooted to the idea of progress (i.e., development) and would be an appropriate component of a theory which sees the system's statuses as genetically determined or as facilitating the conditions for succeeding status to come into play.[8] The mathematical framework we have introduced is also compatible with a "state" notion, in which there is an extensive opportunity to cycle among the statuses. State formulations have been suggested in the psychology literature in relation to anxiety, moods, etc. (e.g., Kessen, 1962, pp. 72-73).

As a final set of considerations in relation to the structure of stage models, we note that all the formulations we have addressed are models of solitary processes. We have proceeded as if intelligence, cognition, motor skills, and personality development unfold autonomously. In reality there

no doubt exist extensive dependencies among some of these processes. Mathematical models of interacting developmental phenomena could be formulated but clear empirically-based specifications of such dependencies are still lacking.

NOTES

[1]The initial condition, $y(0) = 1$, in equation (2) is necessary because diffusion through communication cannot begin until at least one person is knowledgeable.

[2]For a more technical presentation of continuous-time Markov processes see Feller (1968, Chap. 17) and Singer and Spilerman (1974). For discussions on the superimposition of theoretical structures on stochastic models see Coleman (1964, Chaps. 5, 6).

[3]In the present example i, j, k = 1, 2, 3, respectively.

[4]If the observations are on a single individual the interpretation of $p_{ij}(t)$ is in terms of the probability of a stage i to stage j move between times 0 and t.

[5]The symbol "^" over a matrix or over an element in a matrix, will mean that it should be viewed as estimated directly from data rather than calculated from a mathematical model.

[6]We begin here with example 2. Example 1 refers to the structure in Figure 2.

[7]The time-stationary Markov formulations postulate an irrelevance of prior stage affiliations, durations in those stages, and duration in current stage. The last two of these restrictions can be eliminated by introducing non-stationary semi-Markov models as described, for example, in Hoem (1972).

[8]Stages in childhood, such as "walking" or "reading," expose an individual to entirely new sets of experiences which may be prerequisites for the onset of more advanced behaviors.

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